

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/561,874  
Source: IFWP  
Date Processed by STIC: 1/4/06

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IFWP

## RAW SEQUENCE LISTING

DATE: 01/04/2006

PATENT APPLICATION: US/10/561,874

TIME: 10:44:51

Input Set : A:\31304-763.831.txt

Output Set: N:\CRF4\01042006\J561874.raw

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3 <110> APPLICANT: CONARIS research institute AG
4     Seegert, Dirk
5     Schreiber, Stefan
6     Rose-John, Stefan
7     Watzig, Georg H.
8     Rahaus, Nikolas
10 <120> TITLE OF INVENTION: PEGylated soluble gp130-dimers useful as a medicament
12 <130> FILE REFERENCE: 31304-763.831
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/561,874
C--> 15 <141> CURRENT FILING DATE: 2005-12-22
17 <150> PRIOR APPLICATION NUMBER: EP 03 014 049.5
18 <151> PRIOR FILING DATE: 2003-06-23
20 <160> NUMBER OF SEQ ID NOS: 6
22 <170> SOFTWARE: PatentIn version 3.2
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 978
26 <212> TYPE: DNA
27 <213> ORGANISM: homo sapiens
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34 cattctaatt tcaactgcagt ttgtgtgcta aaggaaaaat gtatggatta ttttcatgta   180
36 aatgctaatt acattgtctg gaaaacaaac cattttacta ttcctaagga gcaatatact   240
38 atcataaaca gaacagcatc cagtgtcacc tttaacagata tagcttcatt aaatattcag   300
40 ctcaacttgc acattcttac attcggacag cttgaacaga atgtttatgg aatcacata   360
42 atttcaggct tgcctccaga aaaacctaata aatttgagtt gcattgtgaa cgaggggaag   420
44 aaaatgaggt tggagtggga tgggtggaagg gaaacacact tggagacaaa cttcacttta   480
46 aaatctgaat gggcaacaca caagtttgct gattgcaaag caaaacgtga caccaccacc   540
48 tcatgcactg ttgattatc tactgtgtat ttgtcaaca ttgaagtctg ggtagaagca   600
50 gagaatgcc ttgggaaggt tacatcagat catatcaatt ttgatcctgt atataaagt   660
52 aagcccaatc cgccacataa tttatcagtg atcaactcag aggaactgtc tagtatctta   720
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56 tataggacca aagatgcctc aacttgagc cagattcctc ctgaagacac agcatccacc   840
58 cgatcttcat tcaactgtcca agaccttaaa ccttttacag aatatgtgt taggattcgc   900
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66 <211> LENGTH: 326
67 <212> TYPE: PRT
68 <213> ORGANISM: homo sapiens
70 <400> SEQUENCE: 2
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73 1                               5                               10                               15

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77          20          25          30
80 Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys
81          35          40          45
84 Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr
85          50          55          60
88 Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr
89 65          70          75          80
92 Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser
93          85          90          95
96 Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu
97          100          105          110
100 Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys
101          115          120          125
104 Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys
105          130          135          140
108 Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu
109 145          150          155          160
112 Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg
113          165          170          175
116 Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val
117          180          185          190
120 Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr
121          195          200          205
124 Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro
125          210          215          220
128 Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu
129 225          230          235          240
132 Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Ile Leu Lys
133          245          250          255
136 Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile
137          260          265          270
140 Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp
141          275          280          285
144 Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg Cys Met Lys Glu
145          290          295          300
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149 305          310          315          320
152 Thr Tyr Glu Asp Arg Pro
153          325
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157 <211> LENGTH: 615
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159 <213> ORGANISM: homo sapiens
161 <400> SEQUENCE: 3
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164 cggggcaagt tgccggacgc ccccgagttt gaaaaggatc ttctcattca gagactcaat 120
166 tggatgctat gggatgatcg tgaatgcttc cgcgacctct gttaccgtac cggcatctgc 180
168 aagggtattc tagagcccgc tgctattttt catctgaaac taccagccat caacgatact 240

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170 gatcactgcg ggttaatagg atttaatgag actagctgcc ttaaaaagct cgccgatggc 300
172 ttttttgaat tcgaggtggt gtttaagttt ttaacgacgg agtttggaat atcagtata 360
174 aacgtggacg tcatggagct tctgacgaag accttaggat gggacataca ggaagagctc 420
176 aataagctga ctaagacgca ctacagtcca cccaaatttg accgcggtct attagggagg 480
178 cttcagggac ttaagtattg ggtgagacac tttgcttcgt tttatgttct gagtgcattg 540
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186 <211> LENGTH: 204
187 <212> TYPE: PRT
188 <213> ORGANISM: homo sapiens
190 <400> SEQUENCE: 4
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196 Val Ser Gly Thr Arg Gly Lys Leu Pro Asp Ala Pro Glu Phe Glu Lys
197 20 25 30
200 Asp Leu Leu Ile Gln Arg Leu Asn Trp Met Leu Trp Val Ile Asp Glu
201 35 40 45
204 Cys Phe Arg Asp Leu Cys Tyr Arg Thr Gly Ile Cys Lys Gly Ile Leu
205 50 55 60
208 Glu Pro Ala Ala Ile Phe His Leu Lys Leu Pro Ala Ile Asn Asp Thr
209 65 70 75 80
212 Asp His Cys Gly Leu Ile Gly Phe Asn Glu Thr Ser Cys Leu Lys Lys
213 85 90 95
216 Leu Ala Asp Gly Phe Phe Glu Phe Glu Val Leu Phe Lys Phe Leu Thr
217 100 105 110
220 Thr Glu Phe Gly Lys Ser Val Ile Asn Val Asp Val Met Glu Leu Leu
221 115 120 125
224 Thr Lys Thr Leu Gly Trp Asp Ile Gln Glu Glu Leu Asn Lys Leu Thr
225 130 135 140
228 Lys Thr His Tyr Ser Pro Lys Phe Asp Arg Gly Leu Leu Gly Arg
229 145 150 155 160
232 Leu Gln Gly Leu Lys Tyr Trp Val Arg His Phe Ala Ser Phe Tyr Val
233 165 170 175
236 Leu Ser Ala Met Glu Lys Phe Ala Gly Gln Ala Val Arg Val Leu Asp
237 180 185 190
240 Ser Ile Pro Asp Val Thr Pro Asp Val His Asp Lys
241 195 200
244 <210> SEQ ID NO: 5
245 <211> LENGTH: 915
246 <212> TYPE: DNA
247 <213> ORGANISM: Homo sapiens
249 <400> SEQUENCE: 5
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252 tctaatttca ctgcagtttg tgtgctaaag gaaaaatgta tggattattt tcatgtaaat 120
254 gctaattaca ttgtctggaa aacaaaccat ttactattc ctaaggagca atatactatc 180
256 ataaacagaa cagcatccag tgtcaccttt acagatatag cttcattaaa tattcagctc 240
258 acttgcaaca ttcttacatt cggacagctt gaacagaatg tttatggaat cacaataatt 300
260 tcaggcttgc ctccagaaaa acctaaaaat ttgagttgca ttgtgaacga ggggaagaaa 360

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262 atgaggtgtg agtgggatgg tggaagggaa acacacttgg agacaaactt cactttaaaa 420
264 tctgaatggg caacacacaa gtttgctgat tgcaaagcaa aacgtgacac ccccacctca 480
266 tgcactgttg attattctac tgtgtatttt gtcaacattg aagtctgggt agaagcagag 540
268 aatgcccttg ggaaggttac atcagatcat atcaattttg atcctgtata taaagtgaag 600
270 cccaatccgc cacataattt atcagtgatc aactcagagg aactgtctag tatcttaaaa 660
272 ttgacatgga ccaacccaag tattaagagt gttataatac taaaatataa cattcaatat 720
274 aggaccaaag atgcctcaac ttggagccag attcctcctg aagacacagc atccaccgga 780
276 tcttcattca ctgtccaaga ccttaaacct ttacagaat atgtgtttag gattcgctgt 840
278 atgaaggaag atggtaaggg atactggagt gactggagtg aagaagcaag tgggatcacc 900
280 tatgaagata gacca 915
283 <210> SEQ ID NO: 6
284 <211> LENGTH: 305
285 <212> TYPE: PRT
286 <213> ORGANISM: Homo sapiens
288 <400> SEQUENCE: 6
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291 1 5 10 15
294 Val Gln Leu His Ser Asn Phe Thr Ala Val Cys Val Leu Lys Glu Lys
295 20 25 30
298 Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr Ile Val Trp Lys Thr
299 35 40 45
302 Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr Ile Ile Asn Arg Thr
303 50 55 60
306 Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser Leu Asn Ile Gln Leu
307 65 70 75 80
310 Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu Gln Asn Val Tyr Gly
311 85 90 95
314 Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys Pro Lys Asn Leu Ser
315 100 105 110
318 Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys Glu Trp Asp Gly Gly
319 115 120 125
322 Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu Lys Ser Glu Trp Ala
323 130 135 140
326 Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg Asp Thr Pro Thr Ser
327 145 150 155 160
330 Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val Asn Ile Glu Val Trp
331 165 170 175
334 Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr Ser Asp His Ile Asn
335 180 185 190
338 Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro Pro His Asn Leu Ser
339 195 200 205
342 Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu Lys Leu Thr Trp Thr
343 210 215 220
346 Asn Pro Ser Ile Lys Ser Val Ile Ile Leu Lys Tyr Asn Ile Gln Tyr
347 225 230 235 240
350 Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile Pro Pro Glu Asp Thr
351 245 250 255
354 Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp Leu Lys Pro Phe Thr
355 260 265 270

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358	Glu	Tyr	Val	Phe	Arg	Ile	Arg	Cys	Met	Lys	Glu	Asp	Gly	Lys	Gly	Tyr
359			275					280					285			
362	Trp	Ser	Asp	Trp	Ser	Glu	Glu	Ala	Ser	Gly	Ile	Thr	Tyr	Glu	Asp	Arg
363		290					295					300				
366	Pro															
367	305															

**VERIFICATION SUMMARY**

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Input Set : A:\31304-763.831.txt

Output Set: N:\CRF4\01042006\J561874.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application Number

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date